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LAM, Toong Jin

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XU, Yanfei

HE, Jiangyan

YAN, Tie

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF  
FLUORESCENT TRANSGENIC ORNAMENTAL FISH

<130> 1781-0163P

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<170> PatentIn Ver. 2.0

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<223> CK1

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Met Ser Thr Arg Ser Ile Ser Tyr

1 5

tcc agc ggt ggc tcc atc agg agg ggc tac acc agc cag tca gcc tat 161

Ser Ser Gly Gly Ser Ile Arg Arg Gly Tyr Thr Ser Gln Ser Ala Tyr

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gca gta cct gcc ggc tct acc agg atg agc tca gtg acc agt gtc agg 209

Ala Val Pro Ala Gly Ser Thr Arg Met Ser Ser Val Thr Ser Val Arg

25 30 35 40

aga tct ggt gtg ggt gcc agc cca ggc ttc ggt gcc ggt ggc agc tac 257

Arg Ser Gly Val Gly Ala Ser Pro Gly Phe Gly Ala Gly Gly Ser Tyr

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agc ttg agc agc agc agc atg ggt gga ggc tat gga agt ggt ctt ggt 305

Ser Phe Ser Ser Ser Ser Met Gly Gly Gly Tyr Gly Ser Gly Leu Gly

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Gly Gly Leu Gly Gly Gly Met Gly Phe Arg Cys Gly Leu Pro Ile Thr

75 80 85

gct gta act gtc aac cag aac ctg ttg gcc ccc tta aac ctg gaa atc 401  
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gac ccc aca att caa get gtc cgc act tca gag aaa gag cag att aag 449  
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acc ttc aac aac cgc ttc get ttc ctc atc gac aaa gtg cgc ttc ctg 497  
Thr Phe Asn Asn Arg Phe Ala Phe Leu Ile Asp Lys Val Arg Phe Leu  
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Gln Thr Thr Thr Arg Ser Asn Ile Asp Ala Met Phe Glu Ala Tyr Ile  
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170 175 180

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Glu Leu Glu Ala Lys Val Asp Ala Leu Gln Asp Glu Ile Asn Phe Leu  
235 240 245  
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 Glu Ala Glu Glu Arg Gly Glu Leu Ala Val Lys Asp Ala Lys Leu Arg  
 365 370 375  
 atc agg gag ctg gag gaa get ctt cag agg gcc aag caa gac atg gcc 1265  
 Ile Arg Glu Leu Glu Glu Ala Leu Gln Arg Ala Lys Gln Asp Met Ala  
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 395 400 405  
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 Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser  
 410 415 420  
 aga ctg tcc agc ggt gga gct caa get acc att cat gtt cag cag acc 1409  
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 Tyr Ser Ser Gly Phe Ser Ser Gly Gly Ser Gly Tyr Gly Ser Gly Ser  
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35 40 45  
Gly Phe Gly Ala Gly Gly Ser Tyr Ser Phe Ser Ser Ser Ser Met Gly  
50 55 60  
Gly Gly Tyr Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly Gly Met Gly  
65 70 75 80  
Phe Arg Cys Gly Leu Pro Ile Thr Ala Val Thr Val Asn Asn Leu Leu  
85 90 95  
Ala Pro Leu Asn Leu Glu Ile Asp Pro Thr Ile Ala Val Arg Thr Ser  
100 105 110  
Glu Lys Glu Gln Ile Lys Thr Phe Asn Asn Arg Phe Ala Phe Leu Ile  
115 120 125  
Asp Lys Val Arg Phe Leu Glu Asn Lys Met Leu Glu Thr Lys Trp Ser  
130 135 140  
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145 150 155 160  
Tyr Ile Ser Asn Leu Arg Arg Leu Asp Gly Leu Gly Asn Glu Lys Met  
165 170 175  
Lys Leu Glu Gly Glu Leu Lys Asn Met Gln Gly Leu Val Glu Asp Phe  
180 185 190  
Lys Asn Lys Tyr Glu Asp Glu Ile Asn Lys Arg Ala Ser Val Glu Asn  
195 200 205  
Glu Phe Val Leu Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Asn Lys  
210 215 220  
Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asp Glu Ile Asn Phe Leu  
225 230 235 240  
Arg Ala Val Tyr Glu Ala Glu Leu Arg Glu Leu Gln Ser Ile Lys Asp  
245 250 255  
Thr Ser Val Val Val Glu Met Asp Asn Ser Arg Asn Leu Asp Met Asp  
260 265 270  
Ser Ile Val Ala Glu Val Arg Ala Gln Tyr Glu Asp Ile Ala Asn Arg  
275 280 285  
Ser Arg Ala Glu Ala Glu Ser Trp Tyr Lys Lys Phe Glu Glu Met Gln  
290 295 300  
Ser Thr Ala Gly Gln Tyr Gly Asp Asp Leu Arg Ser Thr Lys Ala Glu  
305 310 315 320  
Ile Ala Glu Leu Asn Arg Met Ile Ala Arg Leu Asn Glu Ile Asp Ala  
325 330 335  
Val Lys Ala Arg Ala Asn Leu Glu Ala Gln Ile Ala Glu Ala Glu Glu  
340 345 350  
Arg Gly Glu Leu Ala Val Lys Asp Ala Lys Leu Arg Ile Arg Glu Leu  
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Glu Glu Ala Leu Gln Arg Ala Lys Asp Met Ala Arg Gln Val Arg Glu  
370 375 380  
Tyr Gln Glu Leu Met Asn Val Lys Leu Ala Leu Asp Ile Glu Ile Ala

385                390                395                400  
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 Gly Tyr Gly Gly Ser Gly Ser Gly Phe Gly Tyr Ser Ser Gly Phe Ser  
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 Ser Gly Gly Ser Gly Tyr Gly Ser Gly Ser Gly Phe Gly Ser Gly Ser  
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Met Pro Phe Gly Asn Thr His Asn Asn

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ttc aag ctg aac tac tca gtt gat gag gag tat cca gac ctt agc aag 160  
 Phe Lys Leu Asn Tyr Ser Val Asp Glu Glu Tyr Pro Asp Leu Ser Lys  
 10                15                20                25

cac aac aac cac atg gcc aag gtg ctg act aag gaa atg tat ggc aag 208  
 His Asn Asn His Met Ala Lys Val Leu Thr Lys Glu Met Tyr Gly Lys

30                35                40

ctt agg gac aag cag acc cca cct gga ttc act gtg gat gat gtc atc 256  
 Leu Arg Asp Lys Gln Thr Pro Pro Gly Phe Thr Val Asp Asp Val Ile

45                50                55

cag act ggt gtt gac aat cca ggc cac ccc ttc atc atg acc gtc ggc 304  
 Gln Thr Gly Val Asp Asn Pro Gly His Pro Phe Ile Met Thr Val Gly

60                65                70

tgt gtt gct ggt gat gag gag tcc tac gat gtt ttc aag gac ctg ttc 352

Cys Val Ala Gly Asp Glu Glu Ser Tyr Asp Val Phe Lys Asp Leu Phe

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90 95 100 105  
cac aag acc gac ctc aac ttt gag aac ctg aag ggt ggt gat gac ctg 448  
His Lys Thr Asp Leu Asn Phe Glu Asn Leu Lys Gly Gly Asp Asp Leu  
110 115 120  
gac ccc aac tac ttc ctg agc agc cgt gtg cgt acc gga cgc agc atc 496  
Asp Pro Asn Tyr Phe Leu Ser Ser Arg Val Arg Thr Gly Arg Ser Ile  
125 130 135  
aag gga tac ccc ctg ccc ccc cac aac agc cgt gga gag cgc aga gct 544  
Lys Gly Tyr Pro Leu Pro Pro His Asn Ser Arg Gly Glu Arg Arg Ala  
140 145 150  
gtg gag aag ctg tct gtt gaa gct ctg agt agc ttg gat gga gag ttc 592  
Val Glu Lys Leu Ser Val Glu Ala Leu Ser Ser Leu Asp Gly Glu Phe  
155 160 165  
aag ggc aag tac tac ccc ctg aag tcc atg act gat gac gag cag gag 640  
Lys Gly Lys Tyr Tyr Pro Leu Lys Ser Met Thr Asp Asp Glu Gln Glu  
170 175 180 185  
cag ctg atc gct gac cac ttc ctc ttt gac aaa ccc gtc tcc ccc ctg 688  
Gln Leu Ile Ala Asp His Phe Leu Phe Asp Lys Pro Val Ser Pro Leu  
190 195 200  
ctg ctg gct gct ggt atg gcc cgt gac tgg ccc gat gcc aga ggc att 736  
Leu Leu Ala Ala Gly Met Ala Arg Asp Trp Pro Asp Ala Arg Gly Ile  
205 210 215  
tgg cac aat gag aac aaa gcc ttc ctg gtc tgg gtg aaa cag gag gat 784  
Trp His Asn Glu Asn Lys Ala Phe Leu Val Trp Val Lys Gln Glu Asp  
220 225 230  
cac ctg cgt gtc att tcc atg cag aag ggt ggc aac atg aag gaa gtg 832  
His Leu Arg Val Ile Ser Met Gln Lys Gly Gly Asn Met Lys Glu Val  
235 240 245  
ttc aag cgc ttc tgc gtt ggt ctt cag agg att gag gaa att ttc aag 880  
Phe Lys Arg Phe Cys Val Gly Leu Gln Arg Ile Glu Glu Ile Phe Lys  
250 255 260 265  
aag cac aac cat ggg ttc atg tgg aac gag cat ctt ggt ttc gtc ctg 928  
Lys His Asn His Gly Phe Met Trp Asn Glu His Leu Gly Phe Val Leu  
270 275 280  
acc tgc ccc tcc aac ctg ggc aca ggc ctg cgc ggt gga gtc cac gtc 976  
Thr Cys Pro Ser Asn Leu Gly Thr Gly Leu Arg Gly Gly Val His Val  
285 290 295  
aag ctg ccc aag ctc agc aca cat gcc aag ttt gag gag atc ctg acc 1024  
Lys Leu Pro Lys Leu Ser Thr His Ala Lys Phe Glu Glu Ile Leu Thr  
300 305 310  
aga ctg cgc ctg cag aag cgt ggc aca ggg ggt gtg gac acc gct tcc 1072  
Arg Leu Arg Leu Gln Lys Arg Gly Thr Gly Gly Val Asp Thr Ala Ser  
315 320 325  
gtt ggt gga gtg ttt gac att tcc aac gct gac cgt atc ggc tct tca 1120  
Val Gly Gly Val Phe Asp Ile Ser Asn Ala Asp Arg Ile Gly Ser Ser  
330 335 340 345  
gag gtt gag cag gtg cag tgt gtg gtt gat ggt gtc aag ctg atg gtg 1168  
Glu Val Glu Gln Val Gln Cys Val Val Asp Gly Val Lys Leu Met Val

350                    355                    360  
 gag atg gag aag aag ctg gga gaa ggc cag tcc atc gac agc atg atc 1216  
 Glu Met Glu Lys Lys Leu Gly Glu Gly Gln Ser Ile Asp Ser Met Ile  
 365                    370                    375  
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 Pro Ala Gln Lys  
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 Val Leu Thr Lys Glu Met Tyr Gly Lys Leu Arg Asp Lys Gln Thr Pro  
 35                    40                    45  
 Pro Gly Phe Thr Val Asp Asp Val Ile Gln Thr Gly Val Asp Asn Pro  
 50                    55                    60  
 Gly His Pro Phe Ile Met Thr Val Gly Cys Val Ala Gly Asp Glu Glu  
 65                    70                    75                    80  
 Ser Tyr Asp Val Phe Lys Asp Leu Phe Asp Pro Val Ile Ser Asp Arg  
 85                    90                    95  
 His Gly Gly Tyr Lys Ala Thr Asp Lys His Lys Thr Asp Leu Asn Phe  
 100                    105                    110  
 Glu Asn Leu Lys Gly Gly Asp Asp Leu Asp Pro Asn Tyr Phe Leu Ser  
 115                    120                    125  
 Ser Arg Val Arg Thr Gly Arg Ser Ile Lys Gly Tyr Pro Leu Pro Pro  
 130                    135                    140  
 His Asn Ser Arg Gly Glu Arg Arg Ala Val Glu Lys Leu Ser Val Glu  
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 Ala Leu Ser Ser Leu Asp Gly Glu Phe Lys Gly Lys Tyr Tyr Pro Leu  
 165                    170                    175  
 Lys Ser Met Thr Asp Asp Glu Gln Glu Gln Leu Ile Ala Asp His Phe  
 180                    185                    190  
 Leu Phe Asp Lys Pro Val Ser Pro Leu Leu Leu Ala Ala Gly Met Ala  
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 Arg Asp Trp Pro Asp Ala Arg Gly Ile Trp His Asn Glu Asn Lys Ala  
 210                    215                    220  
 Phe Leu Val Trp Val Lys Gln Glu Asp His Leu Arg Val Ile Ser Met  
 225                    230                    235                    240  
 Gln Lys Gly Gly Asn Met Lys Glu Val Phe Lys Arg Phe Cys Val Gly  
 245                    250                    255

Leu Gln Arg Ile Glu Glu Ile Phe Lys Lys His Asn His Gly Phe Met  
 260 265 270  
 Trp Asn Glu His Leu Gly Phe Val Leu Thr Cys Pro Ser Asn Leu Gly  
 275 280 285  
 Thr Gly Leu Arg Gly Gly Val His Val Lys Leu Pro Lys Leu Ser Thr  
 290 295 300  
 His Ala Lys Phe Glu Glu Ile Leu Thr Arg Leu Arg Leu Gln Lys Arg  
 305 310 315 320  
 Gly Thr Gly Gly Val Asp Thr Ala Ser Val Gly Gly Val Phe Asp Ile  
 325 330 335  
 Ser Asn Ala Asp Arg Ile Gly Ser Ser Glu Val Glu Gln Val Gln Cys  
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Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn

1 5 10

tat ttt ctg aaa atc atc caa ctg ctg gat gac ttc ccc aag tgt ttc 158

Tyr Phe Leu Lys Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe

15 20 25

atc gtg ggc gca gac aat gtc ggc tcc aag cag atg cag acc atc cgt 206

Ile Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg

30 35 40

ctg tcc ctg cgg ggc aag gcc gtc gtg ctc atg ggg aaa aac acc atg 254

Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met

45 50 55 60

atg agg aag gcc att cgt ggc cac ctg gaa aac aac cca gct ctg gag 302

Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu



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 agg ctg ctt ccc cac atc cgc ggg aac gtg ggc ttc gtc ttc acc aag 350  
 Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys  
 80                      85                      90  
 gag gat ctg act gag gtc cga gac ctg ctg ctg gca aac aaa gtg ccc 398  
 Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro  
 95                      100                      105  
 gct gct gcc cgt gct ggt gcc atc gcc ccc tgt gag gtg act gtg ccg 446  
 Ala Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro  
 110                      115                      120  
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 Ala Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala  
 125                      130                      135                      140  
 ttg gga atc acc acc aag atc tcc aga gga acc att gaa atc ttg agt 542  
 Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser  
 145                      150                      155  
 gac gtt cag ctt atc aaa cct gga gac aag gtg ggc gcc agc gag gcc 590  
 Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala  
 160                      165                      170  
 acg ctg ctg aac atg ctg aac atg ctg aac atc tcg ccc ttc tcc tac 638  
 Thr Leu Leu Asn Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr  
 175                      180                      185  
 ggg ctg atc atc cag cag gtg tat gat aac ggc agt gtc tac agc ccc 686  
 Gly Leu Ile Ile Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro  
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 gag gtg ctg gac atc act gag gac gcc ctg cac aag agg ttc ctg aag 734  
 Glu Val Leu Asp Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys  
 205                      210                      215                      220  
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 Gly Val Arg Asn Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr  
 225                      230                      235  
 ctt gct tcc atc cct cac act atc atc aat gga tac aag agg gtc ctg 830  
 Leu Ala Ser Ile Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu  
 240                      245                      250  
 gct gtc act gtc gaa aca gac tac aca ttc ccc ttg gct gag aag gtg 878  
 Ala Val Thr Val Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val  
 255                      260                      265  
 aag gcc tac ctg gct gat ccc acc gct ttc gct gtt gca gcc cct gtt 926  
 Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val  
 270                      275                      280  
 gcg gca gct aca gag cag aaa tcc gct gct cct gcg gct aaa gag gag 974  
 Ala Ala Ala Thr Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu  
 285                      290                      295                      300  
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 Ala Pro Lys Glu Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly  
 305                      310                      315  
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<210> 6

<211> 319

<212> PRT

<213> Danio rerio

<400> 2

Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn Tyr Phe Leu Lys

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Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe Ile Val Gly Ala

20 25 30

Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg Leu Ser Leu Arg

35 40 45

Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala

50 55 60

Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro

65 70 75 80

His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr

85 90 95

Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg

100 105 110

Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr

115 120 125

Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr

130 135 140

Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu

145 150 155 160

Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn

165 170 175

Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile

180 185 190

Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp

195 200 205

Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn

210 215 220

Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile

225 230 235 240

Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val

245 250 255

Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu

260 265 270

Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr

275 280 285

Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu

290 295 300

Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp

305 310 315

<210> 7

<211> 2241

<212> DNA

<213> Danio rerio

<220>

<221> TATA signal  
<222> (2103)..(2108)  
<220>  
<221> primer bind  
<222> (2221)..(2241)  
<223> CK2  
<220>  
<221> misc feature  
<222> (2142)..(2235)  
<223> Identical to the 5' CK cDNA  
<400> 7

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aattgtctga ctatgcaggg tgtctatgcg tatagtttac agttagacca aagtgtgctg 180  
gtgtgtgaag taacaaatga caaatactca aattgtaatt tactaagtag tttaaaaatg 240  
tagtgcagtg ttgtacttt tatttcaatt ttattctgt ctatgtggat tagacaaatc 300  
acatagaagg taaatcacat cataatgaac agcaaactgt ttgccagcat taaaagaaga 360  
agactgctta gatgcatgct actgatgaga aaataacttt aaacgcacac aagacggcac 420  
gtacccaac gcagtgggga cgttgcaatt gaactcaacg tcaggtcgat gtcaatgttc 480  
ctaataatgt tacagcttga tgttatgcgg ggattatggt tgccatacct gatgaataaa 540  
gggtgcacat tggattttgg tcgctttcca cctatgacat cgttattgga cgtcaaaaata 600  
aatttaggtc accacaacct atatttaacc tgcgtggcaa taactaaatg cactacagaa 660  
taaataatgc agcttttacc agcataatac aaaagctact ttactcat actttgagta 720  
acatttttag gcatgtattg atattttac cagccctccc catacataat cgtatgttta 780  
acattagctt ttttagccgc tagcattact gagcttgtgc atgaaagcag atttgagct 840  
gatgattgcc gtaccatgat ctacacctt gacgattgag taatgtctatt aaatgcccat 900  
attcgtgtt gactgcacg agaaatgaga tgggaacatt tatcagtggc cattaaatac 960  
tattttgtg ttagcttagc tgcagttttt aactattgta attaatgagt ttctcaga 1020  
tgtactttta cttcccttg agtacatttt ccttccttca acctgcagtc actactttat 1080  
agtctgtga ttctgtcca atcaaattgc taccttaaga catgggcat ttataattgc 1140  
tgtcaaaaat atttacacgc attaaccag agatgatgga tgtttactgt atgatgaccg 1200  
aagacgtcaa catggcgta ggttgacgtt tgttagaaa tgaaaattag gttgacgtca 1260  
aacatccaat ctaaaatcat ataatatgt atgttacct tatgacgtct atcagacgtt 1320  
tgtcattatt tgacgttgtt ttaagatgtt acacaacct aatccacca atattaactt 1380  
acaatatcct tagatgtcgg ctgactttg taataatac atcttatgat gttgtgtgcc 1440  
tgttacgttt acacacatgt aaattacatg tcactactta ctactctga gtactttta 1500  
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ctcaagcctc tcttgcatc ctctattcc acctggggca aagccccagg ctgggtgtga 1980  
caacatttat ctaccactt tctctctga cctgtctaac aggtaggggtg tgtgtgagag 2040  
tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtc gctccacct ctcaagagt 2100  
tgtataaaat tggcagcca gctgctgaga gacacgcaga gggactttga ctctccttg 2160  
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actcaaagac acaggatccg g

2241

<210> 8

<211> 1456  
 <212> DNA  
 <213> Danio rerio  
 <220>  
 <221> TATA signal  
 <222> (1389)..(1394)  
 <220>  
 <221> primer bind  
 <222> (1433)..(1456)  
 <223> MCK2  
 <220>  
 <221> misc feature  
 <222> (1428)..(1453)  
 <223> Identical to the 5' MCK cDNA  
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gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca ttttaaata tacttgtctc 60  
 tgtggcttaa tcttgctga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120  
 gcatgtgcac catgacaggc ctgttattca cacttgggtgc catgttggag actgttcggc 180  
 cagctatagt ttcttcaca gagtctggg tcacctaag tcacaaggaa gaaacatgtt 240  
 acatgttaaa atgtgacatt caaattgtag tgcattact aacgaaacgc attacacaag 300  
 ttacagctta aaagattgct agacagaaaa accagggagg gggtttccca taatatccag 360  
 tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420  
 gtgacagaaa accagagatg gaaatacctt ctttgaatt gcataattgc ttaaaagaag 480  
 acacaacagg gatagttcac ccaaaaaaca gaccattctt ttttctgtt gaacaaaaat 540  
 taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600  
 aagtaaatgg gtctccagc atttttcaa tataccttac ttgagttca aaagaaaaac 660  
 acatctcaaa taggtttgag gtgtaataaa cattttcat ttgggggtgg actatcccta 720  
 attatttgac acttaagatt tatagtaaat cattttatag actttctccc ctattaaac 780  
 atggttgaat ttatctcat gtttatgtct ggggtgtgct ttttgaaaa gatttccctg 840  
 tcaaatgttt ttgtgtatgg ttggcgaca atagactgaa ctggcctatc acacagactt 900  
 tcataacaac tccagttgat gcccttcac cctcagtga taaatatggc gtctgacatg 960  
 agcagattaa acacgacact gcaacaact tacctgtaaa aatacaaatt gagtttgcac 1020  
 ccagaatcat gtggtgaacg aagcctacca agagattttt gaaagccatc ggcctgacac 1080  
 ggcgacttct gatatctgtg gtatgtttgg caaaagtgtc gctcagcctt ttagcatgg 1140  
 cagatctccc acatcccatc acccctcctt caacctatc cctcctggaa agctatgtat 1200  
 ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccaca gctgccacct 1260  
 catctaggat gcctggggcc taaattgaag cctttcttac actaaacagg gcataagaga 1320  
 ccagcgccag ccaatcataa ttcagtgagc tctaaaatgg gccagccaat ggctgcaggg 1380  
 gctagaggta tatatatcca aatcaaactc ttcttgctg ggtgaccctt attcggctt 1440  
 ggtgaacagg atccgg

1456

<210> 9  
 <211> 2205  
 <212> DNA  
 <213> Danio rerio  
 <220>  
 <221> primer bind  
 <222> (2179)..(2205)  
 <223> ARP2  
 <220>  
 <221> misc\_feature

<222> (2153)..(2199)

<223> Identical to the 5' ARP cDNA

<220>

<221> intron

<222> (792)..(2152)

<220>

<221> misc\_feature

<222> (775)..(791)

<223> Identical to the 5' ARP cDNA

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atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgatc 60  
attttaattt gtgtgtgata attttacatt ttgtaagtat tttttata aaaaatatat 120  
agaaataata caaatttgtt tacagtattc ttagtatttg caataaacga attttatata 180  
gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240  
tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300  
agataataaa gtgactttt tgggcggacc aaattccctt attaatggc aattcattaa 360  
aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420  
gtgcagattt ttggctgttg ttgaaggga tacatctgcg gccgaaagt aacgggaact 480  
atttacattc ttgtctatta aattatccat tatttgtatt ttattacccc aaccgtaaac 540  
tcaacctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaattgatc 600  
tatattgacc gcagctgtat ctttctaag tgcgactgta caaatacgca ctgaccgtga 660  
cagacacgtg cattgaccaa tcagcgaca gatacgcat tccgcgcga ttctgattgg 720  
atgatcgact gatactaata ttgtccgct tccttcgcg gcctcttct ttacgcgctc 780  
cctaccgtga ggtaaggctg acgccgctct tgtggcgggt tcttaaaatg tgtaataaaa 840  
taacatcata agaggtcacg agaaggctca cgtgtgttta atacagcgg cggttattat 900  
tatgcgttta aagcttgtgt aatgattttt acagtaaaag ttagcactag cctgttagca 960  
caggcctcgt gcgccatgtg tgacgcgacg tttaatagc atctatttg atttgatga 1020  
tccgattctg atattaatca tatttatgcg taaaatgtgt gatgggtctg ctagtggaca 1080  
ttacatgcta gtactgtgc tagtcggctg atccacattg agatgttgcg ctatttgcca 1140  
ttttaaacc agttactctc atttagtga aatattctta agccactaag ttaaatttg 1200  
tcaatcacat ataatttgtt ttatgtttta ttgagtcac cataccaggc aatagtttta 1260  
ttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320  
gtaaaggtaa tcttaagggt gtaaaggctc acccaaaaga caattcacg tcaagtgttt 1380  
tcaaatctta tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440  
accataatac aaatacagga aaaatatact atagaagtcg atggttacag gtttctgca 1500  
ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaaggg 1560  
tgcataaatc agtttctt ttgggtgagc gtctctaaac atttgattta gacacctcag 1620  
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cttctatccc tgtctgtctg catctatga cttgcaggga cgctgtctc agacacgttt 1980  
atagcagtaa atcaaatata atagtctct gattatctt aaatattga aagcttataa 2040  
taggaacca aattacctgg aaacagtta caaacagtaa ttcataattt gtcatttaat 2100  
aagatgcaca caaggcagggt gtaaaagtat tgcttgtgt tgtaatcctc agattttaca 2160  
accttgtctt taaaccggct gttaccgat ccttgaagg gatcc 2205

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Cytokeratin - gene specific primer  
 <400> 10  
 cgctggagta agagatagac ctgg 24  
 <210> 11  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Cytokeratin gene specific primer  
 <220>  
 <221> misc feature  
 <222> (1)..(6)  
 <223> Introduced for restriction site  
 <220>  
 <221> misc feature  
 <222> (3)..(8)  
 <223> BamHI site  
 <400> 11  
 ccggatcctg tgtcttgag ttgctg 26  
 <210> 12  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:  
 Muscle creatine kinase gene specific primer  
 <220>  
 <221> misc feature  
 <222> (3)..(8)  
 <223> BamHI site  
 <400> 12  
 ccggatcctt gggatcagat cctg 24  
 <210> 13  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:  
 Muscle creatine kinase gene specific primer  
 <220>  
 <221> misc feature  
 <222> (1)..(3)  
 <223> Introduced for restriction site  
 <220>  
 <221> misc feature  
 <222> (3)..(B)  
 <223> BamHI site  
 <400> 13

ccggatcctg ttcaccaagc cgaa 24

<210> 14

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Acidic ribosomal protein PO gene specific primer

<400> 14

tagttggact tccacgtgcc ctgtc 25

<210> 15

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Acidic ribosomal protein PO gene specific primer

<220>

<221> misc feature

<222> (1)..(7)

<223> Introduced for restriction site

<220>

<221> misc feature

<222> (1)..(6)

<223> BamHI site

<400> 15

ggatcccttc caaggatcgg tgaaca 26

<210> 16

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide for linker used in linker-mediated PCR

<400> 16

gttcatcttt acaagctagc gctgaacaat gctgtggaca agcttgaatt c 51

<210> 17

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide for linker used in linker-mediated PCR

<220>

<223> n is a dideoxycytidine

<400> 17

gaattcaagn 10

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

linker specific primer

<400> 18

gttcattctt acaagctagc g 21

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

linker specific primer

<400> 19

tcctgaacaa tgctgtggac 20

<210> 20

<211> 1392

<212> DNA

<213> Danio rerio

<220>

<221> CDS

<222> (42)..(551)

<220>

<221> primer bind

<222> (6)..(28)

<223> M2

<220>

<221> primer bind

<222> (23)..(45)

<223> M1

<220>

<221> polyA signal

<222> (797)..(802)

<220>

<221> polyA\_signal <222> (1351)..(1357)

<400> 20

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Met Ala Pro Lys Lys

1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104

Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser

10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152

Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile

25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200

Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp

40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248

Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu



55                      60                      65  
 gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296  
 Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu  
 70                      75                      80                      85  
 acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344  
 Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile  
 90                      95                      100  
 gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag 392  
 Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys  
 105                      110                      115  
 aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc 440  
 Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr  
 120                      125                      130  
 gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct 488  
 Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala  
 135                      140                      145  
 ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag 536  
 Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu  
 150                      155                      160                      165  
 gag aag gag gag taa acaacctgg aatagaggaa acgaagagaa gaacatgcat 591  
 Glu Lys Glu Glu  
 170

cctcacagct taatctccag tctgtgtct ggccttctct aacttttgtt ttctctcct 651  
 ccctttcttg ctttctacca tcgtgtgtac tccaagcact tacactctcc atcttaccaa 711  
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<210> 21

<211> 169

<212> PRT

<213> Danio rerio

<400> 21

Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser  
 1                      5                      10                      15  
 Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys  
 20                      25                      30  
 Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys  
 35                      40                      45  
 Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys  
 50                      55                      60  
 Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn

65                      70                      75                      80  
 Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp  
                     85                      90                      95  
 Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly  
                     100                      105                      110  
 Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln  
                     115                      120                      125  
 Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe  
                     130                      135                      140  
 Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val  
 145                      150                      155                      160  
 Ile Thr His Gly Glu Glu Lys Glu Glu  
                     165

<210> 22

<211> 2054

<212> DNA

<213> Danio rerio

<220>

<221> TATA signal

<222> (1983)..(1989)

<220>

<221> enhancer

<222> (142)..(148)

<223> E-box, canntg

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<221> enhancer

<222> (452)..(457)

<223> E-box, canntg

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<221> enhancer

<222> (1095)..(1100)

<223> E-box, canntg

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<221> enhancer

<222> (1278)..(1283)

<223> E-box, canntg

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<222> (1362)..(1367)

<223> E-box, canntg

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<221> enhancer

<222> (1385)..(1390)

<223> E-box, canntg

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<221> enhancer

<222> (523)..(532)

<223> Potential MEF2 binding site, yta(w)4tar

<220>

<221> enhancer

<222> (606)..(615)  
 <223> Potential MEF2 binding site, yta(w)4tar  
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 <222> (697)..(706)  
 <223> Potential MEF2 binding site, yta(w)4tar  
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 <222> (1640)..(1649)  
 <223> Potential MEF2 binding site, yta(w)4tar  
 <220>  
 <221> enhancer  
 <222> (1956)..(1965)  
 <223> Potential MEF2 binding site, yta(w)4tar  
 <220>  
 <223> Transcription start site at residue 2012  
 <220>  
 <221> primer bind  
 <222> (2032)..(2054)  
 <223> M2  
 <220>  
 <221> misc difference  
 <222> (2027)..(2054)  
 <223> Identical to the 5' MLC2f cDNA  
 <409> 22  
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